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MOFFICE S	18
	GTT
	GCT

CGA GTA AGT ATG GCT GTT Arg Val Ser Met Ala Val

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CTG	Leu	
AIG ICI	Ser	
ATG	Met	
GGA	Gly	
$_{ m LLL}$	Phe	
CIC CIC CIC IIA I	Leu	
CIC	Leu	
CIC	Leu	
CTC	Leu	
GCT	Ala	-20
CTT	Phe Leu Ala	
TTC	Phe	
AGT	Ser	
GTT	Val	
AGA	Arg	
CAC	His	

114 AAC Asn Leu 5 ACC CysAla GCT Lys 1 GCC AAG A.sp GAT GCA Ala CAT His Glu GAA GIG Val AAT Asn AGC Ser Leu

162 AAG Lys Glu GAA GAA Glu 20 TCA Arg CGTPro CCCCys IGC Val 15 GLL GGA G1yTAT gaa gaa Ala Arg 10 AGA CCA Pro Asp GAT IGI

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210 Cys GGT GlyAAG Lys ACG GGC G1yGCA Ala TGC CysTGT Cys AAC Asn ACC Thr TGC. Cys ATA Ile CGG Arg Asp GAT Asn AAG

258 GAT Ser GAG Glu GGA G1yGAA Glu IGI CysGLL Val LLL Phe Thr ACT G1*Y* 45 GAT GAT AGI Ser TTCPhe TAC AAG

Figure 1a

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•	306	354	402	450	4 9 8	546	
	CCT AGA AAT CCA AAG GCT TGT ACC TTA AAC TGT GAT CCA AGA ATT GCC Pro Arg Asn Pro Lys Ala Cys Thr Leu Asn Cys Asp Pro Arg Ile Ala 55	TAT GGA GTT TGC CCG CGT TCA GAA GAA AAG AAG AAT GAT CGG ATA TGC Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys 75	ACC AAC TGT TGC GCA GGC ACG AAG GGT TGT AAG TAC TTC AGT GAT GAT Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys Lys Tyr Phe Ser Asp Asp Asp 90	GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT CCT AGA AAT CCA AAG GCT Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala 110	TGT CCT CGG AAT TGC GAT CCA AGA ATT GCC TAT GGG ATT TGC CCA CTT Cys Pro Arg Asn Cys Asp Pro Arg Ile Ala Tyr Gly Ile Cys Pro Leu 120	GCA GAA GAA AAG AAT GAT CGG ATA TGC ACC AAC TGT TGC GCA GGC Ala Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly 135	8

Figure 1b

<u>m</u>	594	642	069	738	786	834	ر ا
	AAA AAG GGT TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT GTT TGT GAA Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu 155	GGA GAG TCT GAT CCT AAA AAT CCA AAG GCC TGT CCT CGG AAT TGT GAT Gly Gly Ser Asp Pro Lys Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp 170	GGA AGA ATT GCC TAT GGG ATT TGC CCA CTT TCA GAA GAA AAG AAG AAT Gly Arg ile Ala Tyr Gly ile Cys Pro Leu Ser Glu Glu Lys Lys Asn 190	C GCA GGC AAA AAG GGT TGT AAG TAC S Ala Gly Lys Lys Gly Cys Lys Tyr 210	TTT AGT GAT GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT CCT AAA Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Lys 215	AAT CCA AAG GCT TGT CCT CGG AAT TGT GAT GGA AGA ATT GCC TAT GGG Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly 235	

3/21

Figure 1c

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	888	930	978	1026	1074	1122	
	TCA GAA GAA AAG AAT GAT CGG ATA TGC ACA AAC Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn 255	AAA AAG GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr 270	GGA GAG TCT GAT CCT AGA AAT CCA AAG GCC TGT CCT Gly Glu Ser Asp Pro Arg Asn Pro Lys Als Cys Pro 290	GGA AGA ATT GCA ATT TGC CCA CTT TCA GAA Gly Arg ile Ala Tyr Gly ile Cys Pro Leu Ser Glu 300	GAT CGG ATA TGC ACC AAT TGT TGC GCA GGC AAG AAG Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys 315	TTT AGT GAT GGA ACT TTT ATT TGT GAA GGA GAA Phe Ser Asp Asp Gly Thr Phe Ile Cys Glu Gly Glu 335	
	CTT Leu 250	GGC	GAA Glu	GAT Asp	AAT Asn	TAC Tyr 330	
	GC CCA	GC GCA rs Ala 265	T TGT 11 Cys	AAT TGT Asn Cys	G AAG 'S Lys	T AAG s Lys	
	ATT TGC Ile Cys	TGT TGC Cys Cys	TTT GTT Phe Val 280	CGG AA Arg As 295	GAA AAG Glu Lys	GGC TGT Gly Cys	
C)						

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Figure 1d

	ב
TCT GAA TAT GCC AGC AAA GTG GAT GAA TAT GTT GGT GAA GTG GAG AAT Aer Glu Tyr Ala Ser Lys Val Asp Glu Tyr Val Gly Glu Val Glu Asn 345	1170
GAT CTC CAG AAG TCT AAG GTT GCT GTT TCC TAAGTCCTAA CTAATAATAT Asp Leu Gln Lys Ser Lys Val Ala Val Ser 360	1220
GTAGTCTATG TATGAAACAA AGGCATGCCA ATATGCTCTG TCTTGCCTGT AATCTGTAAT	1280
ATGGTAGTGG AGCTTTTCCA CTGCCTGTTT AATAAGAAAT GGAGCACTAG TTTGTTTTAG	1340
TIAAAAAAA AAAAAAAA	1360

Figure 1e

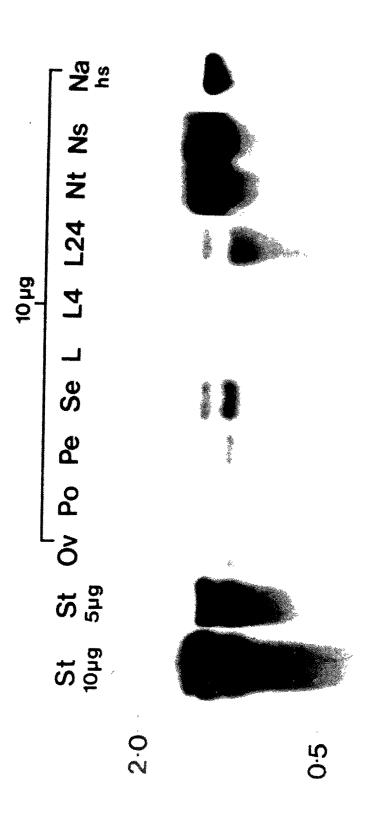


Figure 2

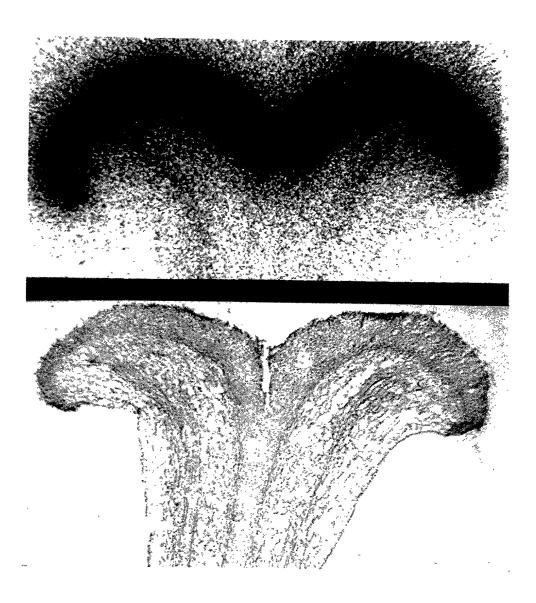
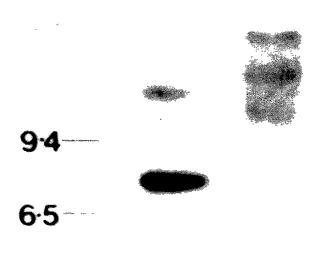


Figure 3

EcoRI HindIII



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Figure 4

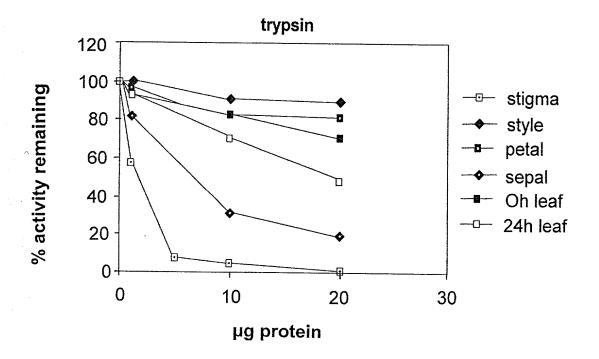


Figure 5a

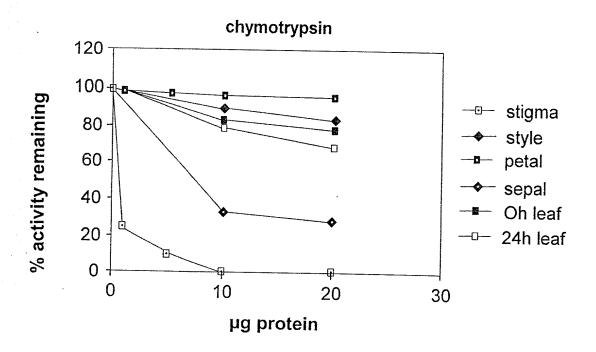


Figure 5b

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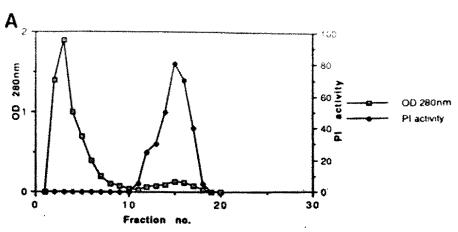


Figure 6b

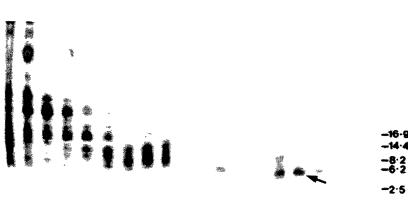
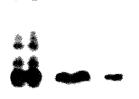


Figure 6c

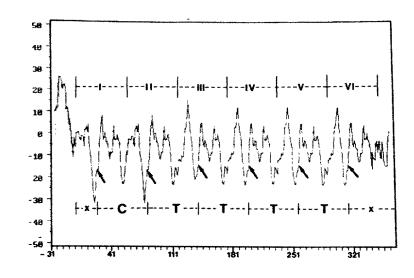
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2 - 3



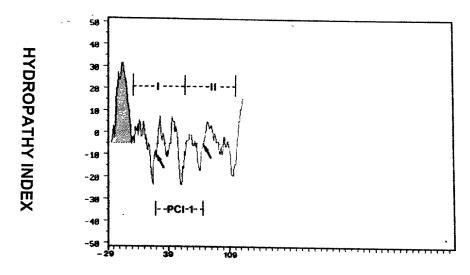
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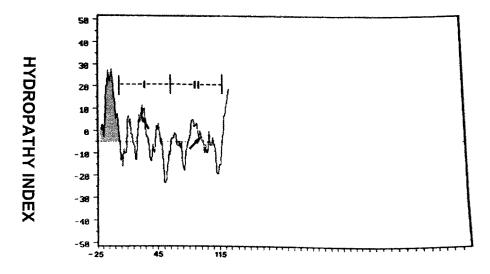
AMINO ACID RESIDUE NUMBER

Figure 7a



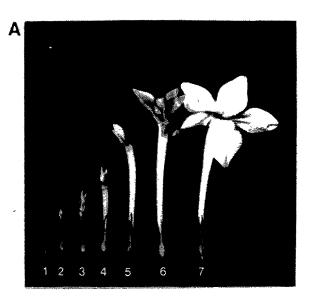
AMINO ACID RESIDUE NUMBER

Figure 7 b



AMINO ACID RESIDUE NUMBER

Figure 7c



"福度证据"

Figure 8b

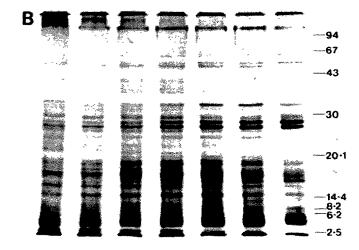
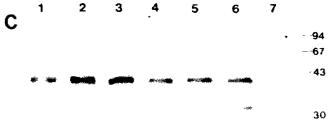


Figure 8 c



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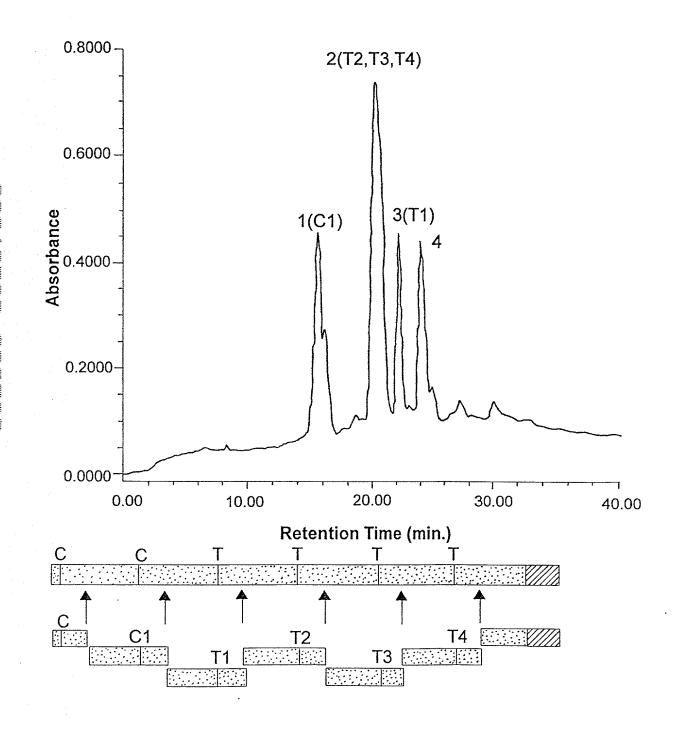


Figure 9a

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DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRS
                                                                        DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPL
```

DRICTNCCAGREGCKYFSDDGTFVCEGESDPENPKACPRNCDGRIAYGICPLS

DRICTNCCAGKKGCKYFSDDGTFVCEGESDPKNPKACPRNCDGRIAYGICPLS DRICTNCCACKKGCKYFSDDGTFVCEGESDPRNPKACPRNCDCRIAYGICPLS

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Figure 9b

Figure 10

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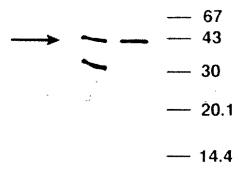


Figure 11a

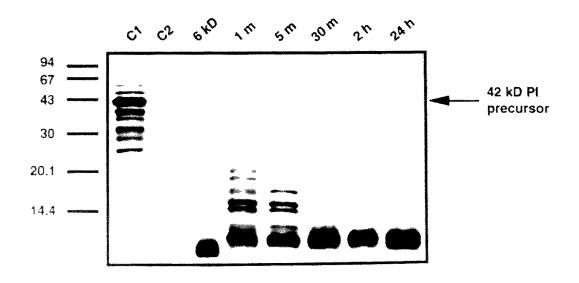


Figure 11 b

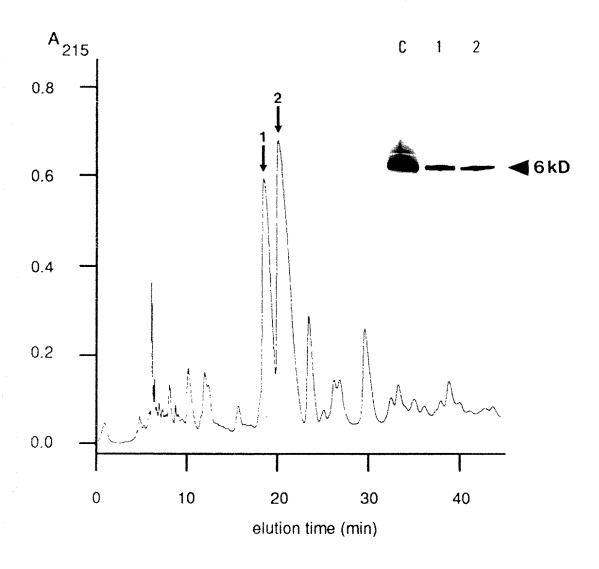


Figure 12

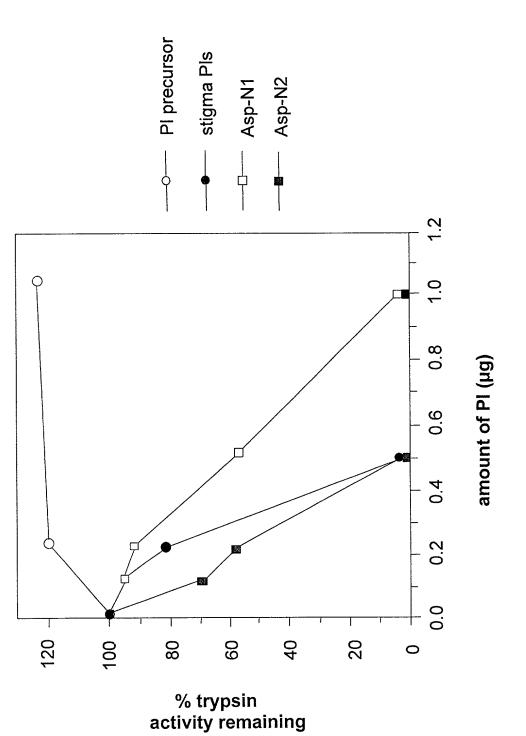
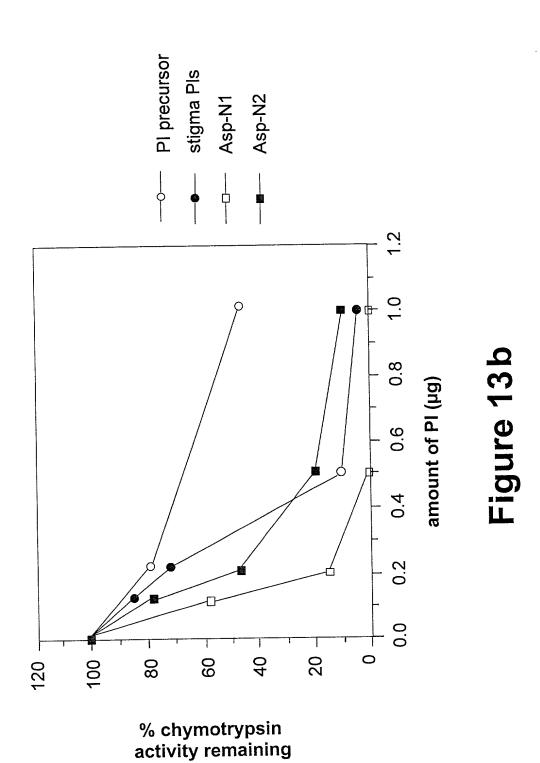
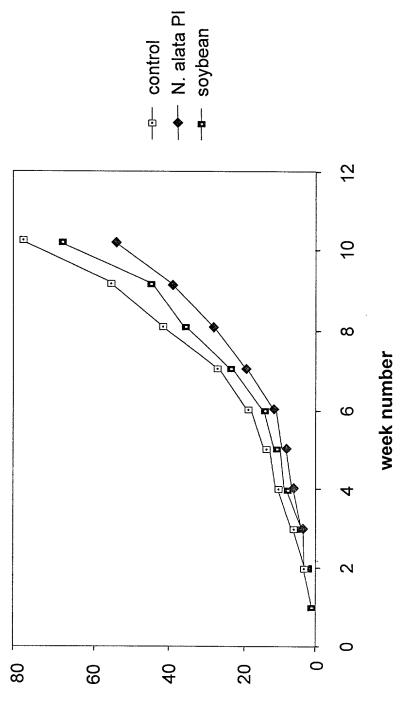


Figure 13a





mean weight (+/-s.e.m.;mg)